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(54) Modification of plant viruses or their effects.

(57) The invention relates to a method of modifying a plant virus or its effects, which comprises incorporating genetic material into a plant and infecting said plant with a plant virus, whereby expression of the incorporated genetic material modifies the plant virus or its effects. In a preferred embodiment, expression in the plant of the incorporated genetic material causes attenuation of the symptoms of attack on the plant by a plant virus.

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MODIFICATION OF PLANT VIRUSES OR THEIR EFFECTS

This invention relates to the modification of plant viruses or their effects.

The particles of some cultures of cucumber mosaic virus (CMV) contain, in addition to the three genomic species of single-stranded RNA and a sub-genomic species that acts as mRNA for CMV particle protein, another single-stranded linear RNA molecule that typically is about 335 nucleotides long. This extra molecule, known as satellite RNA, does not share any appreciable nucleotide sequence with CMV genomic RNA but replicates only in plants or protoplasts that are infected with CMV. CMV isolates that do not contain satellite RNA can be cultured repeatedly in plants in a satellite-free state, but when satellite RNA is added to such cultures it is synthesized and persists as a component of the virus isolate. The effect of satellite RNA on CMV infections varies between strains. In many cases the normal symptoms of CMV are suppressed and as a result the infected plants show no obvious signs of infection. However, the presence of other strains of satellite RNA leads to the production of severe symptoms which are quite distinct from those of CMV.

Since plants containing infections of CMV with some strains of satellite RNA show milder symptoms than infections without satellite, it has been proposed to use complete viruses containing satellite RNA to protect plants against the effects of CMV infections. Experiments have in fact shown that pre-infection with a CMV strain containing satellite RNA causes protection against CMV symptoms and leads to increased yield of pepper plants. It has also been shown that infection of tomato plants with CMV strains containing a benign satellite RNA results in a cross protection against the effects of CMV strains with a virulent satellite RNA. However, the use of a complete virus as the prophylactic agent may cause several problems. The protecting strain may itself have adverse effects on growth and yield or may be a reservoir for infection of other plant species. It is also possible that the avirulent strain may mutate to virulence.

We have sought to eliminate these difficulties by the strategy demonstrated in this invention in which biologically active, preferably virus-derived genetic material, in particular satellite RNA, is maintained in the plant by transcription from the nuclear genome.

The present invention provides a method of modifying a plant virus or its effects, which comprises incorporating genetic material into a plant and infecting said plant with a plant virus, whereby expression of the incorporated genetic material modifies the plant virus or its effects.

The genetic material to be incorporated is preferably derived, optionally with modification, from a plant virus which is the same as or different from the plant virus which is to infect the plant.

In a preferred embodiment, expression in the plant of the incorporated genetic material causes attenuation of the symptoms of attack on the plant by a plant virus.

The genetic material transferred into the plant is preferably cDNA corresponding to plant viral satellite RNA, the cDNA and/or the satellite RNA optionally having been modified.

Expression of viral RNA may protect the plant against the pathogenic effects of a related viral RNA. Alternatively, expression of RNA of viral origin may protect against the pathogenic effects of a viral RNA which does not have sequence homology. It should also be noted that the expression of viral genetic material, as RNA, may exert its effect independently of the translation of that RNA into protein.

The invention also provides a method of genetically engineering a plant, which comprises incorporating into the nuclear genome of the plant DNA which is capable of being expressed in the plant and capable upon challenge of the plant by a plant virus, of modifying said plant virus or its effects. The invention further relates to a plant which has been genetically engineered by such a method, as well as the progeny of such a plant.

Viruses which are particularly suitable for use in the invention are those having relatively low molecular weight satellite RNA, generally with less than 1000 nucleo tides. Examples are Cucumber Mosaic Virus, or other cucumoviruses, Tobacco Ringspot Virus, or other nepoviruses, Tomato Bushy Stunt Virus or other tombusviruses, Turnip Rosette Virus and sobemoviruses or other viruses allied to them. Any plants which can be infected by such viruses can be used in the invention.

Preferably the virus is cucumber mosaic virus (CMV) and the genetic material used for transformation is cDNA corresponding to CMV satellite RNA. The cDNA is preferably transferred into an expression vector which allows transfer of DNA into the nuclear genome of a recipient plant, for example an expression vector based on the Ti plasmid system of Agrobacterium tumefaciens.

The invention thus also provides an expression vector capable of transferring DNA into the nuclear genome of a recipient plant, characterised in that it incorporates transferable DNA capable of being expressed in the recipient plant and capable, upon challenge of the plant by a plant virus, of modifying said plant virus or its effects. The expression vector

is preferably a plasmid including the T-DNA border sequences from a Ti plasmid of Agrobacterium tumefaciens, a transcriptional promoter, cDNA corresponding to CMV satellite RNA, and a transcriptional terminator.

Cells of the plant to be protected, e.g. leaf disks, are infected by a strain of A. tumefaciens harbouring the expression vector and whole plants are generated from infected cells which have been transformed.

It has been shown in several laboratories that the Ti plasmid of Agrobacterium can be used to introduce novel DNA sequences into the nuclear DNA of plants. It has further been shown that if these DNA sequences contain appropriate promoter and terminator sequences, then the DNA is transcribed into RNA in the transformed cells. Any other methods and vectors for the introduction of novel DNA sequences and which are not related to Agrobacterium are also suitable for use in this invention, provided that a transcriptional promoter and transcriptional terminator are incorporated into the vector molecule as an expression cassette for the appropriate viral sequence. The use of direct DNA uptake methods for the transformation of plant cells is also possible and has been shown in the following articles:

Krens, F. et al. Nature 296, 72-74 (1982)
Paskowski, J et al. EMBO J. 3, 2717-2722 (1984)
Hains, R. et al. Mol. Gen. Genet. 199, 161-168 (1985)
Potrykus et al. ibid. 199, 183-188 (1985)
Fromm et al. Nature, 319, 791-793 (1986)

We have demonstrated that satellite RNA multimers are processed into unit length molecules and subsequently replicated if co-infected into tobacco plants with CMV-RNA. This observation was important because the methods of achieving expression of novel DNA as RNA in transformed cells require that the RNA transcripts include sequence from the transcriptional terminator and promotor regions. Work on other viral systems had suggested that addition of foreign sequence to the termini of viral RNA molecules affected the ability of that RNA to replicate. In the absence of proof that the satellite RNA could be generated by processing from a multimer, it seemed that the most likely outcome of an experiment in which a cDNA copy of satellite RNA was expressed as RNA in transformed cells was that the transcript would not be replicated by the incoming virus. Since the action of satellite RNA in inhibition of viral symptoms is likely to be mediated by competition between satellite and viral RNA for replication machinery, this would imply that the satellite transcript in the transformed cells would not affect CMV symptom production.

However, having established that satellite RNA could be processed from multimers it became evident that biologically active satellite RNA could be expressed in transformed plant cells. The primary transcription product would be multimeric satellite RNA molecules containing additional sequence at the termini from the promoter and from the transcriptional terminator. It was predicted that, either before or following CMV infection, the satellite multimer transcript would be processed into unit length molecules which would then undergo normal satellite RNA activity in CMV infected cells. This activity would, it was predicted, include replication and symptom attenuation. This description outlines the construction of cDNA clones containing satellite RNA as multimeric structures and the insertion of these sequences into a Ti plasmid expression vector. The biological activity of multimer transcripts of satellite RNA has been demonstrated in cells of transformed tobacco.

Reference is now made to the accompanying drawings, in which:

Figure 1 shows the nucleotide sequence of cDNA corresponding to CMV satellite RNA;

Figure 2 is an outline scheme for the construction of satellite cDNA multimers;

Figure 3 is the detailed structure of the CMV satellite cDNA molecules in the binary Ti plasmid expression vectors;

Figure 4 is a Northern blot analysis of RNA from transformed plants;

Figure 5 shows the effect of CMV infection on the occurrence of satellite RNA in transformed plants; and

Figure 6 shows the effect of transcribed satellite on symptom production.

EXAMPLES

In order to illustrate an embodiment of the invention we describe the transformation of tobacco plants with DNA copies of CMV satellite RNA, the production of satellite RNA transcripts by such plants and the acquisition of satellite RNA by CMV cultures grown in them.

The satellite RNA used in this work was isolated from CMV strain $I_{17}N$ (ref 20) and was cloned a complementary DNA (cDNA). The nucleotide sequence of the cDNA clone was very similar to that of other strains of CMV. Two head-to-tail concatemeric satellite cDNA molecules were constructed. These comprised one (pT104) or two (pT105) complete satellite RNA sequence units with incomplete units at the 5′ end (Fig. 3) and were intended to mimic multimeric satellite RNAs which are thought to be replication intermediates. To achieve expression of these satellite sequences in

transformed plants, the cDNA molecules were transferred into an expression vector (RokI) based on the binary Ti plasmid system of Agrobacterium tumefaciens. The resultant plasmids are referred to as RokI/104 and RokI/105.

The description is in four parts: isolation and purification of satellite RNA; cloning of satellite RNA as cDNA; construction of satellite cDNA multimers; transfer of satellite cDNA into a Ti plasmid.

ISOLATION AND PURIFICATION OF SATELLITE RNA

Plants of Nicotiana clevelandii were infected with cucumber mosaic virus (strain $I_{17}N$, provided by Dr. M. Jacquemond, INRA, Montfavet, France) and the virus particles isolated and purified exactly as described by Lot et al. (ref 1). RNA was extracted from virus particles by the addition of sodium dodecyl sulphate to 1%, extraction with buffer saturated phenol (50 mM Tris-HCl pH8) and ethanol precipitation. The RNA was recovered by centrifugation and was resuspended at 0.5 mg ml^{-1} in water. Satellite RNA was purified by sucrose gradient centrifugation. 33 µg of CMV RNA was diluted to 100 µl of H_2O and 2µl of 1M Tris-Borate buffer (pH8) was added with 5 µl of 1M methyl mercuric hydroxide. After 5 min at room temperature 5 µl of β-mercaptoethanol was added and the sample was loaded onto a 5-20% (w/v) sucrose gradient in tubes of a Sorvall AH650 rotor. The gradient was buffered with 10 mM Tris-HCl pH 7.5, 100 mM NaCl, 1 mM ethylene diamine tetraacetic acid (EDTA) pH8. The gradient was centrifuged for 2h at 50000 rpm at 20°C and 20 equal volume fractions were collected by dripping from the bottom. Aliquots (20 µl) from each fraction were assayed by electrophoresis in an agarose gel which was stained with ethidium bromide to detect the presence of satellite RNA. The fractions which contained satellite RNA were combined and the satellite RNA was collected by ethanol precipitation and dissolved in 20 µl of distilled water.

CLONING OF SATELLITE RNA AS COMPLEMENTARY DNA (cDNA)

To facilitate priming of cDNA synthesis, a polyadenylate sequence was added to the 3' end of the satellite RNA. 10 µl of the satellite RNA was incubated in 25 µl of 25 mM Tris-HCl pH 7.9 250 mM NaCl with 2.5 mM $MnCl_2$, 500 µM ATP, 15 U of placental ribonuclease inhibitor and 0.2 U of poly A polymerase for 15 min at 37°C. The reaction was terminated by dilution to 75 µl and extraction with phenol. The polyadenylated satellite was then precipitated twice with ethanol and resuspended in 10 µl of distilled water.

The synthesis of cDNA from this RNA was primed with oligo dT_{12-18}in a reaction volume of 25 µl which contained 25 mM Tris-HCl pH 8.3, 10 mM KCl, 4 mM $MgCl_2$, 0.025 mg ml^{-1} oligo dT_{12-18}, 5 mM dithiothreitol, 500 µM each of dATP, dGTP, dCTP and TTP, 15 U of placental ribonuclease inhibitor, 15 U of reverse transcriptase and 10 µCi of ^{32}P (α labelled) dATP (≃ 500 Ci mmol) (New England Nuclear). After 1 h at 42°C the reaction was boiled for 1 min, cooled on ice for 10 min and centrifuged at 10000 x g for 10 min. The supernatant was added to 2.5 µl of 1M HEPES buffer pH7, 0.5 µl each of 20 mM dATP, dGTP, dCTP and TTP, 1.5 µl of 0.1M KCl, 2.6 µl of water and 5U of DNA polymerase 1 (Klenow fragment). The DNA was then passed through a 1 ml column of Sephadex G-50, ethanol precipitated and resuspended in 50 µl of 0.3 M NaCl, 0.03M NaOAc (pH 4.5), 4.5 mM$ZnSO_4$, 5% glycerol containing 3000U ml^{-1} of S1 nuclease. After 1 h at 37°C the reaction was diluted by the addition of 50 µl TE and the sample layered over a 5-20% sucrose gradient in 10 mM Tris-HCl pH 7.5, 1 mM EDTA, 100 mM NaCl and centrifuged for 4 h at 50000 rpm in a SORVALL AH 650 rotor. The gradient was fractionated from the bottom and the largest 50% of cDNA molecules, detected by monitoring radioactivity in fractions, were pooled into one fraction. The sample was extracted with phenol/chloroform, precipitated with ethanol and collected by centrifugation at 40000 rpm for 30 min in a SORVALL AH 650 rotor. The samples were reprecipitated with ethanol from 100 µl, rinsed with ethanol and dried and dissolved in 10 µl of 1 mM Tris-HCl pH8, 0.1 mM EDTA.

The cDNA was then incubated with terminal transferase and dCTP, to add oligo dC tails which would facilitate cloning of the cDNA into the plasmid vector. The reactions contained 5 µl of cDNA, 1 µl of 10 x buffer (1.4 M cacodylic acid, 0.3 M Tris base, 1.1 M KOH), 0.2 µl of 10 mM dCTP, 0.1 µl of 20 µM dithiothreitol, 1.7 µl of water, 1 µl of 10 mM $CoCl_2$ and 10 U of terminal transferase. The reaction was incubated for 10 minutes at 37°C and then stopped by incubation at 65°C for 2 minutes.

The vector for cloning was the plasmid pUC9 (ref 2) which was digested with PstI and tailed with dGTP in a similar reaction with terminal transferase. The tailed cDNA (4 µl) was annealed with tailed plasmid (80 ng) in 30 µg of 10 mM Tris-HCl pH 7.4, 100 mM NaCl, 0.1 mM EDTA. The reaction was heated to 65°C and cooled to 4°C overnight. Aliquots (5 µl) of the annealing mix were transformed into E. coli strain MC1022 and plated onto

ampicillin with indicators (1PTG and Xga1) for the presence of a cDNA insert in the LacZ gene. Colonies showing no blue colour were selected for further analysis.

Initially the plasmid DNA was analysed for the presence of an insert which hybridised to purified satellite RNA. Subsequently, having confirmed this, plasmid DNA was purified and the size of the insert was determined by digestion with PstI and electrophoresis in polyacrylamide.

For one of the clones, designated B7, the insert size was shown to be approximately 410 bp. This indicated that the cDNA insertion would contain most or all of the satellite sequence (335 bp), combined with the homopolymer tails added as described above to facilitate cloning.

To confirm the extent of the cDNA in the insert of B7, the nucleotide sequence was determined using the method of Maxam and Gilbert (ref 3) and is shown in Fig. 1. The sequence was very similar to that of other CMV satellite RNA molecules determined directly from the RNA, exept that 3 nucleotides at the 5′ end were absent from the cDNA, presumably as a result of incomplete copying by reverse transcriptase.

The subsequent manipulations could be carried out with clones showing different degrees of completeness at the 5′ end, except that different oligonucleotide reagents (see page 13) would be used to compensate.

CONSTRUCTION OF SATELLITE cDNA MULTIMERS

For the reasons described in the introductory section, it was considered necessary to construct multimeric copies of the satellite cDNA. These were a complex series of manipulations outlied in Fig. 2 in which the aims were to, firstly remove the homopolymer tails from the 3′ of the satellite sequence. The cDNA molecules were then constructed with a dimeric structure, which included at the junction between the two satellite sequences, the 5′ homopolymer tail. The next step was to clone out the junction region and, using oligonucleotide directed mutagenesis techniques to remove the 5′ homopolymer tail, and to replace the missing 3 nucleotides from the 5′ end. The modified junction region was then joined to a restriction fragment containing the satellite cDNA to create structures which contained one or two complete units of satellite sequence. These manipulations are described in more detail below.

a) Removal of homopolymer tails from the 3′ of the satellite sequence.

This was achieved using Bal 31 nuclease. First 60 µg of the plasmid B7 was rendered linear by cutting with BamHI. B7 contains a single BamHI site which is located adjacent to the PstI site where the cDNA was inserted, and on the 3′ side of the insertion. The DNA was then phenol extracted, ethanol precipitated and suspended in 400 µl of 10 mM Tris-HCl (pH 8) 1 mM EDTA. 100 µl of Bal 31 buffer was added and 0.5 U of Bal 31 nuclease. 130 µl aliquots were removed at 8, 12, 16 minutes and extracted with phenol. The DNA was then collected by ethanol precipitation. The ends of the Bal 31 digested DNA were treated with T4 DNA polymerase in order to remove overhanging 3′ ends and to fill in recessed 3′ ends. The reaction contained TA buffer (33 mM Tris-acetate pH 7.9, 66 mM K acetate, 10 mM Mg acetate, 4 mM spermine, 0.5 mM dithiothreitol), 2.5 µM of dATP, dGTP, dCTP and TTP and 5U of T4 DNA polymerase in 75 µl. After 3 h at 37°C the reaction was diluted to 100 µl and the DNA digested with PstI to release two fragments. The larger one was the vector plasmid deleted from the BamHI site. The smaller was the cDNA inserts extending from the 5′ PstI site to the site of the Bal 31 deletion. In order to isolate the deleted cDNA molecules extending approximately to the terminal nucleotides of the cDNA insert (...CCC_{OH}) and not into the homopolymer tails, the DNA was fractionated on a 5% polyacrylamide gel and the cDNA fragments of approximately 350 nucleotides were isolated. These fragments were then cloned into pUC9 which had been digested with PstI and SmaI. Since the terminal nucleotides of the cDNA represent the 5′ nucleotides of a SmaI site, the clones containing a deletion to the precise 3′ end of the cDNA could be recognised by the presence of a SmaI site in the recombinant plasmid. One clone, designated D26 was identified which met this criterion. The presence of the correct insert was confirmed by digestion with other restriction enzymes. The insert of this clone was transferred to another plasmid, pSP6/4 (ref 4) for the purposes of another experiment although this was not essential for the manipulations described here. Subsequent manipulations were based on the construction of D26 in pSP6/4, which was designated pSP102. The relevant features of pSP102 are shown in Fig. 2.

b) Mutation of junction region.

The next step involved the addition of a second satellite cDNA insertion into pSP102 to create a head to tail dimer structure. To do this, the insert of pSP102 was released by digestion of 10 µg DNA with SmaI and PstI. The protruding 3' end of the PstI site was rendered blunt by the addition of dATP, dGTP, dCTP and TTP to 100 µM and 4 U of T4 polymerase in 25 µl. Following incubation at 37°C for 15 minutes the cDNA insert was purified by fractionation on a 5% polyacrylamide gel. This cDNA insertion was then cloned into the SmaI site of pSP102 and the resultant clones were screened for the presence of an insertion in the head to head, or head to tail configuration by digestion with TaqI. One clone with the head to tail dimer was designated pSP103.

In order to mutate the junction region of the dimer so that the homopolymer tail was removed, and so that the 5' nucleotides thought to be missing from the cDNA were restored, it was necessary to clone the junction region clones into a single stranded phage vector, mp10 (ref 5). It was also necessary to obtain a synthetic oligonucleotide which represent the complement of the sequence in the corrected junction. This oligonucleotide was purchased from Dr. S. Minter (UMIST) and was the sequence TCCATCAAACAAAACGGGTCCTGTGTAGGA (within this the sequence GGG is the complement of the 3' end of the satellite RNA and the sequence AAAAC the complement of the 5' end of the satellite, including the missing nucleotides).

The DNA of pSP103 extending between the TaqI sites, shown in Fig. 2 was cloned into mp10, at the Acc1 site. Single stranded DNA from this clone, which was designated Taq3, was isolated by standard procedures (ref 5).

The synthetic oligonucleotide was prepared for use by reaction with ATP and polynucleotide kinase. The rection contained 15 pmol of oligonucleotide, 70 mM Tris.HCl pH 7.6, 10 mM $MgCl_2$, 5 mM dithiothreitol, 1 mM ATP and 10 U of polynucleotide kinase in 20 µl. The reaction was incubated at 37°C for 1 h and stopped by heating at 70°C for 10 min.

The kinase oligonucleotide (5 pmol) was then annealed to 2 µg of DNA from Taq3 with 25 ng of sequence primer (a synthetic oligonucleotide with the sequence GTAAAACGACGGCCAGT, obtained from New England Biolabs) with 10 mM Tris-HCl pH8, 1 mM EDTA in a reaction volume of 12 µl. The reaction was initiated at 80°C in a 250 ml beaker of water which was then cooled to 15°C on ice. To this was then added the following: 1 µl of 100 mM Tris-HCl pH8, 10 mM $MgCl_2$,1µl of 5 mM dATP, dGTP, dCTP and TTP, 1 µl of 5 mM ATP, 1 µl 0.1M dithiothreitol, 4µl of water, 1 U of DNA polymerase I (Klenow fragment) and 6 U of T4 DNA ligase. The reaction was incubated for 4 h at 15°C and diluted with 180 µl of 10 mM Tris-HCl pH8, 1mM EDTA, 1 µl aliquots of this were transformed into E. coli (strain JM101).

The resultant plaques were hybridised with the synthetic (junction sequence) oligonucleotide, labelled with ^{32}P in order to detect clones containing the mutated (corrected) junction region. The mutated clones were distinguished from non-mutated clones by increased stability of the resultant hybrids.

To label the synthetic oligonucleotide, the reaction contained 15p mol of oligonucleotide, 200 µCi of ^{32}P labelled (γ position) ATP (3000 Ci mmol), 70 mM Tris-HCl pH 7.6, 10 mM $MgCl_2$, 5 mM dithiothreitol and 10 U of polynucleotide kinase. The reaction was incubated at 37°C for 30 min and heated at 70°C to stop the reaction. For the hybridisation step, a replica of the phage plaques was formed on a nitrocellulose filter by layering the filter on the plaques for 30 sec. The filter (9 cm diameter) was then floated on 0.5N NaOH, 0.5M NaCl for 1 min and twice for 1 min on 1.5M NaCl, 0.5M Tris HCl pH 7.5. The filter was then baked in vacuo at 80°C for 2 h, prehybridised in 1M NaCl, 33 mM PIPES pH 6.8, 6.6 mM EDTA, 0.2% gelatin, 0.2% Ficoll, 0.2% polyvinylpyrollidone 360, 0.1% sodium dodecyl sulphate for 1 h at 65°C and then hybridised with the ^{32}P oligonucleotide (1.5 pmol) in 1 ml of 1 M NaCl, 33 mM PIPES pH 6.8, 6.6 mM EDTA for 16 h at 25°C. The filter was then rinsed several times in 0.9M NaCl, 0.09M sodium citrate and autoradiographed to detect the hybridisation. The filter was then washed at 42°C, 52°C, 62°C and 72°C in 0.9M NaCl, 0.09M sodium citrate and the hybridisation was monitored by autoradiography in between each temperature step.

Of the plaques showing stable hybridisation at 62°C and 72°C, six were selected and cultured. Single stranded DNA was prepared by standard procedures (ref 5), and the sequence across the junction region was confirmed using the dideoxy sequencing method of (ref 6). These clones were designated Taq 3'.

To build up the multimeric satellite units containing this corrected junction region it was necessary to obtain sufficient quantities of the DNA in double stranded form. This was achieved by cloning the TaqI fragment containing the junction region from Taq 3' into a plasmid vector. The single stranded Taq 3' DNA (25 µl) was incubated in 75 µl with 40 ng of sequencing primer defined above and 10 µl of 100 mM Tris-HCl pH8, 10 mM Mg Cl_2 at 65°C for 1 h. To this was added 20 µl of 5 mM dATP, dGTP, dCTP, TTP and 25 U of DNA polymerase I (Klenow fragment). After incubation at 20°C for 30 min the sample was digested with EcoRI and HindIII (50 U each) and incubated at

37°C for 1 h. These enzymes excised the Taq 3′ DNA adjacent to either side of the junction fragment cDNA. The released junction fragment was subsequently purified by polyacrylamide gel electrophoresis and cloned into plasmid vector pUC9. One clone containing the desired fragment of Taq 3′ was identified by restriction enzyme digestion and designated pUS1.

c) Construction of satellite multimers.

To construct a cDNA containing the junction fragment of pUS1 joined to a cDNA fragment extending from the TaqI[a] site through to the 3′ terminus of the satellite DNA, the following manipulations were carried out.

First the ScaI/SstI fragment of pSP102 and the BamHI/ScaI fragments of pUS1 were isolated by polyacrylamide gel electrophoresis and ligated together with vector DNA (pT7/2, ref 7) digested with BamHI and SstI. The choice of vector was determined by a different experiment. Other vectors (e.g. pUC9) could have been substituted for this. The clones containing the correct insertion of the two fragments from pUS1 and pSP102 were identified by restriction enzyme digestion with BamHI and SstI (producing the inserted cDNA of approximately 450 nucleotides). One of these was designated pT104.

Although the prediction, outlined in the introduction was that multimeric transcripts would be processed in transformed plants, it was not possible to predict from the information available the precise constructions which would be necessary to produce this result. For example, if the sequence determining the processing reaction is contained internally to the processed unit then expression of the pT104 construction would be adequate. If, however, the necessary sequence is located externally to the processed unit then it would be necessary to express a multimeric transcript which contained satellite cDNA sequence on both sides. For this reason a further construction was made containing two complete satellite units flanked on the 5′ side by an incomplete unit.

In order to make this construction the pT104 and the pUS1 DNAs were digested with TaqI under conditions where plasmid molecules were excised, on average, once per molecule. The digested DNA was then fractionated on a 0.7% agarose gel and the full length linear molecules were isolated. The pT104 DNA was then digested with SstI and fractionated on a 5% polyacrylamide gel in order to isolate fragments of the size predicted (approximately 450 bp) for the distance between TaqI[a] site and the SstI site (Fig. 2). Similarly, pUS1 was digested with BamHI and fragments were isolated to the size predicted (approximately 350 bp) for the BamHI/TaqI[b]fragment (Fig. 2). These fragments were combined, ligated with pT7-2 digested with BamHI and SstI and transformed into E. coli. Several clones were identified containing the desired insertion and one of these was designated pT105.

TRANSFER OF SATELLITE cDNA MULTIMERS INTO A Ti PLASMID

To obtain expression of satellite sequences in transformed plants the cDNA insertions of pT104 and pT105 were transferred into an Agrobacterium Ti plasmid vector called RokI, which was obtained from M. Bevan. This is based on the vector Bin 19, described previously (ref 8), containing additionally a promoter and transcriptional terminator, and a BamHI site between these from insertion of new sequence. The promoter and terminator were as described previously (ref 9) in a vector constructed for the expression of a viral coat protein in transformed cells, with the difference that the promoter of RokI contained 6 nucleotides on the 3′ side of the transcriptional initiation point, whereas the promoter used previously contained 132 bp in this region.

The RokI DNA (5 µg) was digested with BamHI in 40 µl and then treated with T4 DNA polymerase 5 U and 100 µM each of dATP, dGTP, dCTP and TTP for 15 min at 37°C and 10 min at 65°C. To this was then added 0.6 U of calf intestinal phosphatase and the DNA was incubated at 37°C for 60′. Following treatment at 65°C for 10 min the DNA was extracted with phenol and precipitated with ethanol. The pT104 and pT105 DNAs were digested with BamHI and EcoRI and treated in a volume of 50 µl with 2.5 U of DNA polymerase I (Klenow fragment) with 50 µM each of dATP, dGTP, dCTP and TTP for 15 min at 37°C. The DNA was then fractionated on a 5% polyacrylamide gel and the satellite cDNA insertions were isolated.

Figure 3 shows the detailed structure of the CMV satellite cDNA molecules in the binary Ti plasmid expression vectors. At the 5′ of the 104 construction there are 51 nucleotides from the polylinker of plasmid pT7-2 extending from the transcriptional start point and including polylinker sequences of pT7-2 and other vectors used in the construction of pT104. On the 3′ end of this as shown in the diagram there are 98 nucleotides extending from position 227 of the satellite sequence through to the 3′ nucleotide of the satellite unit at position 335 ("TE 3′"). Immediately 3′ of this there is a complete satellite unit, in the same orientation as the incomplete unit, flanked at the 3′

end by 16 nucleotides extending between the SmaI site and the EcoRI site of vector plasmid pT7-2 (ref 7). The 105 construction is as 104, except that two complete satellite units, in the same orientation, are present. The insertions from 104 and 105 were excised by digestion with restriction endonucleases BamHI and EcoRI, rendered blunt ended by the action of DNA polymerase (Klenow fragment) and inserted into the BamHI site of binary Ti plasmid RokI. The BamHI site of RokI was rendered flush ended by the action of DNA polymerase (Klenow fragment). RokI is a derivative of the binary vector Bin19, described previousiy (ref 8), containing additionally an expression cassette inserted into the polylinker site. The expression cassette comprised the promotor of cauliflower mosaic virus 35S RNA (ref 10) and the terminator fragment of the nopaline synthase (nos) gene of Agrobacterium T-DNA (ref 11) (NOS TERM). It is essentially similar to the expression cassette described for the expression of tobacco mosaic virus coat protein gene (ref 9) except that the promoter fragment was deleted back to 6 bp 3′ of the cap site of the 35S transcript using Bal31 nuclease. The unique BamHI site was inserted between the promoter and terminator fragments. Transcripts derived from this cassette would contain 10 nucleotides from the promoter and 200 nucleotides from the terminator (ref 11) in addition to the sequence inserted at the BamHI site.

The figure shows only the region adjacent to the cDNA insert of pT104 and pT105 and the expression cassette region of RokI.

The digested RokI DNA was then ligated separately with the insertion of pT104 or p105 and transformed into E. coli. Recombinant clones were identified by digestion with EcoRI and HindIII (see Fig. 3 for location of these sites) and the plasmids containing the required insertions designated RokI/104 or RokI/105 respectively. These plasmids were then transferred into Agrobacterium by mating as described (ref 8). The resultant Agrobacterium strains were then used to transform cells in leaf discs of Nicotiana tabacum (var Samsun NN) using exactly the procedure of Horsch et al. (ref 12) except that (i) the leaves used were from axenically-grown plants, and were not sterilised; (ii) the selection of transformed plant cells was on 100 μg ml^{-1} kanamycin.

Mature plants were regenerated from the transformed plants, also as described by Horsch et al. (ref 12).

The analysis of these plants is described below.

Transformed tobacco plants (cv. Samsun NN) were regenerated from Agrobacterium-infected leaf disks and were assayed for the presence of the satellite sequence in DNA and RNA by Southern and Northern blot analysis, respectively. The Southern blot analysis showed that the DNA of transformed plants contained the equivalent of 1-3 copies of the satellite cDNA per haploid genome. It was also shown, by Southern blot analysis, that the cDNA sequence, the promoter site and the RNA termination site had not been rearranged or deleted. The Northern blot analysis (Fig. 4) showed transcripts of about 700 nucleotides (RokI/104) or 1000 nucleotides (RokI/105), which are the approximate sizes predicted from the location of promoter and terminator sequences in the original constructions (Fig. 3) and allowing for the presence of a 3′ polyadenylate tract. These RNA molecules were readily detected in total RNA or in polyadenylated RNA. No virus-like symptoms or other abnormalities in growth, flowering or seed production were observed in the transformed plants. Figure 4 is a Northern blot analysis of RNA from transformed plants.

Total RNA (20 μg) or poly A^+ RNA (1 μg) was isolated from leaves of non-transformed plants (non-trans) or plants transformed with RokI/104 and RokI/105 and fractionated on formaldehyde/agarose gels. The transcribed satellite RNA sequences were detected by blotting the gel onto nitrocellulose and hybridisation with nick translated insert from pT105. Total RNA from cells infected with CMV which contained satellite RNA was included as a reference for satellite RNA unit length (1X) and dimer length (2X) molecules. The size markers were virion RNA of CMV, which was detected with a cDNA clone (C20) of CMV genomic RNA (DCB, unpublished). This hybridised with CMV RNA-3, CMV RNA-4 and faintly with CMV RNA-1 and RNA-2. The size values given are those of Gould and Symons (ref 13). **Methods.** The constructions of 104 and 105 in RokI were mobilised into Agrobacterium strain LBA 4404 using E. coli strain HB101 harbouring pRK2013 in a triparental mating, as described (ref 8). The resultant Agrobacterium strains containing the binary vector constructions were then used to infect leaf disks from axenically grown Nicotiana tabacum (cv. Samsun NN). The infected and transformed cells were regenerated into plants by culturing the disks successively on a layer of tobacco feeder cells and then on shoot and root inducing medium as described by Horsch et al.(ref 12) The shoot and root induction media contained kanamycin at 100 μg ml^{-1} to select for cells expressing the neomycin phosphotransferase gene contained in the T-DNA region of RokI (from Bin19) (ref 8). Transformed plants were propogated by transfer of stem cuttings into root induction medium.

RNA isolations were as described by Apel and Kloppstech[27] (ref 14) and electrophoresis and blotting analysis as described by Goldberg (ref 15) and Thomas (ref 16). Figure 5 shows the effect of CMV infection on the satellite RNA in transformed plants.

Leaves of transformed or non-transformed N. tabacum (var. Samsun NN) were inoculated with CMV strain R76B and 35 mm disks were cut 5 h later. Batches of 5 disks were floated on SPS medium (10 g l^{-1} sucrose, 0.2 g l^{-1} Ca $(H_2PO_4)_2.H_2O$, 0.3 g l^{-1} sulphanilamide). Total RNA (1 µg) was isolated from these samples, or as indicated below, and analysed by Northern blotting as described for Fig. 4 using as probes the insert of pT105 (satellite RNA) or C20 (CMV RNA). The size markers were RNA of tissue infected with CMV alone (tracks 1 and 26) or CMV with satellite (tracks 18, 19 and 27) to show CMV RNA-1, CMV RNA-2, CMV RNA-3 and CMV RNA-4 or satellite monomer (1X) or dimer units (2X).

a) RNA in primary infections. Tracks 2-4 show RNA from disks of non-transformed plants , inoculated with CMV R76B and sampled at 5 h (track 2) post inoculation or 4 d (track 3) and 7 d (track 4) of incubation. Tracks 5 and 6 show RNA from disks of mock inoculated (non-transformed) plants at 4 d (track 5) or 7 d (track 6) incubation. Tracks 7-9 show RNA from a plant transformed with RokI/C20. This is similar to RokI/104 (Fig. 3) except that the insertion at the BamHI site of RokI was cDNA (C20) of the coat protein mRNA of CMV. The RNA was isolated at 5 h after infection (track 7) or from disks incubated for 4 d (track 8) and 7 d (track 9). Tracks 10-13 and 14-17 contain RNA from plants transformed with RokI/104 or RokI/105 respectively. The RNA was isolated before infection (tracks 10 and 14), 5 h after infection (tracks 11 and 15) and from disks at 4 d (tracks 12 and 16) and 7 d (tracks 13 and 17) of incubation.

b) RNA in secondary infections. Extracts of CMV-infected leaf disks, similar to those described in the experiment of Fig. 5a, were inoculated onto Nicotiana clevelandii. RNA was isolated from the systemically infected tissue after 10 days. The RNA (1 µg) was isolated from plants inoculated with extracts of disks of plants transformed with RokI/C20 (tracks 20-22), RokI/104 (track 23) or RokI/105 (tracks 24, 25).

c) RNA in CMV particles. Disks from CMV (R76B)-infected plants transformed with RokI/105 were extracted at 7 d of incubation and the inoculum passaged through non-transformed N. clevelandii and re-inoculated onto N. clevelandii. After ten days of infection CMV particles were isolated from systemically infected leaves and the viral RNA extracted by addition of sodium dodecyl sulphate to 1% and treatment with phenol. Total cellular RNA was also isolated from this tissue for comparison. The samples shown are 100 ng virion RNA (track 33) or total cellular RNA (2.9 µg, track 28; 0.7 µg, track 29; 0.29 µg, track 30; 0.07 µg, track 31; 0.029 µg, track 32).

To determine the biological activity of these transcribed RNA molecules, the transformed plants were infected with CMV strain R76B. This is a satellite-free isolate of CMV obtained originally from a naturally infected raspberry plant in Scotland (ref 17). In one such test, disks were cut from leaves 5 h after inoculation. RNA was isolated from the disks, either at that time, or after floating the disks on SPS medium for 4 or 7 days. Northern blot analysis of the RNA with a probe for CMV (C20) (Fig.5a) showed that by 4 days the CMV genomic RNAs had accumulated in disks both from the transformed and non-transformed plants. Many small RNA species which may represent subgenomic RNA species (ref 18) also accumulated over the same period (Fig. 5a). Satellite RNA was detected by Northern blot analysis after 4 days and 7 days but only in the disks from plants transformed with RokI/104 or RokI/105 (Fig. 5a). This RNA was present in large amounts and was primarily of unit satellite RNA length although, as is normal for an infection containing satellite, some dimers were also detected (Fig. 5a).At the loading of RNA and autoradiographic exposure of Fig. 5a, the transcribed satellite RNA molecules of about 700 and 1000 nucleotides were not detectable. The faint hybridisation of the satellite probe to high molecular weight RNA on some tracks of this gel is an artifact of aggregation of the probe with ribosomal RNA.

In further tests, sap from the disks sampled 4 and 7 days after inoculation was itself inoculated to Nicotiana clevelandii. Ten days after inoculation, RNA was isolated from the systemically infected leaves of these plants. Satellite RNA was detected by Northern blot analysis, in amounts typical of natural satellite RNA, and in unit and dimeric lengths, but only where the inoculum had been obtained from CMV-infected discs from plants transformed with RokI/104 or RokI/105 (Fig. 5b). The CMV probe detected viral genomic RNA in all samples (Fig. 5b).

In a similar experiment, a virus culture from CMV-infected plants which had been transformed with RokI/105 was propagated twice in N. clevelandii and RNA was then isolated from CMV particles purified from these plants. Again unit and dimer length satellite RNA was detected in amount typical of a preparation containing natural satellite (Fig. 5c) although the amount of dimer was depleted in virions relative to the amount in total cellular RNA.

Unit and dimer length of satellite RNA were detected at high levels in extracts of systemically infected leaves, from CMV-inoculated plants which had been transformed with RokI/104 and RokI/195. Satellite RNA was not detected in extracts from systemically infected leaves of comparable non-transformed plants.

Clearly the transcribed satellite RNA in transformed plants can be processed to unit length molecules following CMV infection and subsequently acquired and perpetuated as a new part of the virus culture.

The ability to produce transcribed satellite RNA was inherited by the progeny of the plants transformed with RokI/104 and RokI/105. This was shown by Northern blot analysis of the poly A+ RNA in the F1 progeny of these transformed plants, exactly as described above for the primary transformed plants (see reference to Northern blot analysis of Fig. 4).

F1 progeny of the transformed plants which had inherited the expression cassette with satellite cDNA and the associated DNA from the RokI vector were selected for this analysis by germination on MS medium (1 litre of MS medium contains 4.6 g Murashige and Skoog salt mixture (Flow Lab. cat no. 26-330-24), 0.1 g inositol, 0.01 g thiamine-HCl, 0.001 g nicotinic acid, 0.001 g pyridoxine HCl, 30 g sucrose, 7.0 g agarose at a final pH of 5.8) containing 1 micro g per ml kanamycin. The plants which carry the kanamycin resistance gene, originally derived from RokI/105 or RokI/104, are identifiable in this selection procedure as they show normal leaf greening and only slightly retarded leaf development. Tobacco plants which do not carry the kanamycin resistance gene fail to develop normal roots or green leaves. The kanamycin resistant seedlings were transferred from the kanamycin medium to soil or potting compost as soon as differential growth was observed between the kanamycin resistant seedlings and seedlings which had not inherited an active kanamycin resistance gene. The transcribed satellite produced in the F1 progeny plants was biologically active in the same way as the satellite RNA of the primary transformants. This was shown by infecting the F1 progeny plants with satellite RNA free virus (cucumovirus, see below) which caused the transcribed satellite RNA of the F1 progeny plants to be processed and replicated as unit length satellite RNA molecules which accumulated to a high level in the systemically infected leaves and which could be propagated as part of the virus culture during passage onto non-transformed plants. These effects were demonstrated using the methods described for the primary transformed plants (see reference above to Fig. 5b).

The transcribed satellite RNA was replicated as unit dimer length molecules, as described above, not only by CMV strain R76B, but also by other strains of cucumber mosaic virus. This was shown by infecting the transformed plants or their F1 progeny with CMV strain KIN or with CMV strain Y. CMV-KIN was isolated from a natural plant infection in Kinnaird, near Dundee and CMV-Y was obtained as RNA from Dr. Takanami of the Japan Tobacco and salt public Corporation, Umegaoka, Yokohama 227, Japan. A virus related to CMV, tomato aspermy virus (TAV) was also effective in causing the replication of transcribed satellite RNA. However, peanut stunt virus, which is distantly related to CMV, or brome mosaic virus, which is classed in a separate viral group from cucumber mosaic virus, were both not capable of causing the replication of transcribed satellite RNA.

The accumulation of satellite RNA in the transformed plants caused the properties of CMV infections to be modified on those plants. This was shown for CMV-R76B or CMV-KIN, inoculated onto either the primary transformed plants or onto the F1 progeny of those plants and by analysis of the viral RNA in the systemically infected leaves. In the plants producing transcribed satellite RNA the proportion of cellular RNA which has virus genomic RNA was less than 20% of the level in infected plants which were not producing transcribed satellite. The methods used to show this involved Northern blot analysis as described above.

A second way in which the presence of transcribed satellite caused a modification of the CMV infection was shown in transformed plants which were inoculated with CMV-KIN and tomato aspermy virus. In these instances the symptoms of viral disease were much attenuated in the plants producing transcribed satellite RNA compared with non-transformed plants, or transformed plants which were not producing transcribed satellite RNA. This illustrated in Fig. 6, which is an illustration of plants transformed with RokI/104 and RokI/105 and of non-transformed plants at approximately 4 weeks after infection with tomato aspermy virus. The effect was most obvious in the systemically infected leaves in which the mosaic and leaf distortions produced by the tomato aspermy virus were absent from the plants producing transcribed satellite RNA. Transformed plants or non-transformed plants were inoculated with tomato aspermy virus and photographed 4 weeks after infection. a) shows the intact plants and b) systemically infected leaves. 104 and 105 are the transformed plants expressing satellite, as described above. 30K is a transformed plant, expressing a sequence of tobacco rattle virus and is a control to show that transformation per se has no effect on symptom production. NT is a non-transformed plant.

This symptom attenuation effect with TAV was independent of the strength of the inoculum and the length of the infection up to six weeks post-inoculation, which is the latest time tested. The effect was highly reproducible, being observed in all of the plants producing transcribed satellite which were tested.

CMV or TAV cultures which acquired satellite RNA as as result of passage through plants which were producing transcribed satellite RNA also showed modified properties. This was demonstrated when Nicotiana clevelandii plants were inoculated with CMV or TAB which had been passaged through various tabacco plants as described above with reference to Fig. 5b. The disease symptoms were reduced markedly when the inoculum had been passaged through plants which were producing transcribed satellite RNA.

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Claims

1. A method of modifying a plant virus or its effects, which comprises incorporating genetic material into a plant and infecting said plant with a plant virus, whereby expression of the incorporated genetic material modifies the plant virus or its effects.

2. A method according to claim 1, in which the genetic material to be incorporated is derived, optionally with modification, from a plant virus which is the same as or different from the plant virus which is to infect the plant.

3. A method according to claim 1 or 2, in which expression in the plant of the incorporated genetic material causes attenuation of the symptoms of attack on the plant by a plant virus.

4. A method according to any of claims 1 to 3, in which the genetic material is cDNA corresponding to plant viral satellite RNA, the cDNA and/or the satellite RNA optionally having been modified.

5. A method according to claim 3 or 4, in which the genetic material is derived from a symptom-attenuating satellite RNA.

6. A method according to any of claims 3 to 5, in which the genetic material is derived from an RNA which can be processed from a multimeric structure.

7. A method according to any of claims 1 to 6, in which the genetic material is derived from satellite RNA of a virus selected from cucumoviruses, nepoviruses, tombusviruses, sobemoviruses and other viruses allied to them.

8. A method according to claim 7, in which the virus is Cucumber Mosaic Virus, Tobacco Ringspot Virus, Tomato Bushy Stunt Virus or Turnip Rosette Virus, or any virus allied to them.

9. A method according to any of claims 1 to 8, in which the virus is Cucumber Mosaic Virus (CMV) and the genetic material used for transformation is cDNA corresponding to CMV satellite RNA.

10. A method according to any of claims 4 to 9, wherein the cDNA is transferred into the plant using an expression vector which allows transfer of DNA into the nuclear genome of a recipient plant.

11. A method according to claim 10, wherein the expression vector is based on the Ti plasmid system of Agrobacterium tumefaciens.

12. A method according to claim 11, in which the expression vector is a plasmid including the T-DNA border sequences from a Ti plasmid of Ag-

robacterium tumefaciens, a transcriptional promoter, cDNA corresponding to plant viral satellite RNA, and a transcriptional terminater.

13. A method according to claim 11 and 12, wherein cells of the plant to be transformed are infected by a strain of A. tumefaciens harbouring the expression vector and whole plants are regenerated from infected cells which have been transformed.

14. An expression vector capable of transferring DNA into the nuclear genome of a recipient plant, characterised in that it incorporates transferable DNA capable of being expressed in the recipient plant and capable, upon challenge of the plant by a plant virus, of modifying said plant virus or its effects.

15. An expression vector according to claim 14, in which the transferable DNA is cDNA corresponding to plant viral satellite RNA, the cDNA and/or the satellite RNA optionally having been modified.

16. An expression vector according to claim 14 or 15 and based on the Ti plasmid system of Agrobacterium tumefaciens.

17. A method of genetically engineering a plant, which comprises incorporating into the nuclear genome of the plant DNA which is capable of being expressed in the plant and capable upon challenge of the plant by a plant virus, of modifying said plant virus or its effects.

18. A plant which has been genetically engineered by the method of claim 17, or the progeny of such a plant.

```
*TY CMVSAT.LIS
 GTTTTGTTTG ATGGAGAATT GCGCAGAGGG GTTATATCTG CGTGAGGATC TGTCACTCGG
          10         20         30         40         50         60

 CGGTGTGGGA TACCTCCCTG  CTAAGGCGGG TTGAGTGATG TTCCCTCGGA  CTGGGGACCG
          70         80         90        100        110        120

 CTGGCTTGCG AGCTATGTCC  GCTACTCTCA  GTACTACACT CTCATTTGAG CCCCCGCTCA
         130        140        150        160        170        180

 GTTTGCTAGC AGAACCCGGC  ACATGGTTCG  CCGATACCAT GGAATTTCGA AAGAAACACT
         190        200        210        220        230        240

 CTGTTAGGTG GTATGAGTCA TGACGCACGC  AGGGAGAGGC TAAGGCTTAT GCTATGCTGA
         250        260        270        280        290        300

 TCTCCGTGAA TGTCTATCAT TCCTACACAG  GACCC
         310        320        330          5         15         25

 DIR CMV*
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Fig.1.

0 242 016

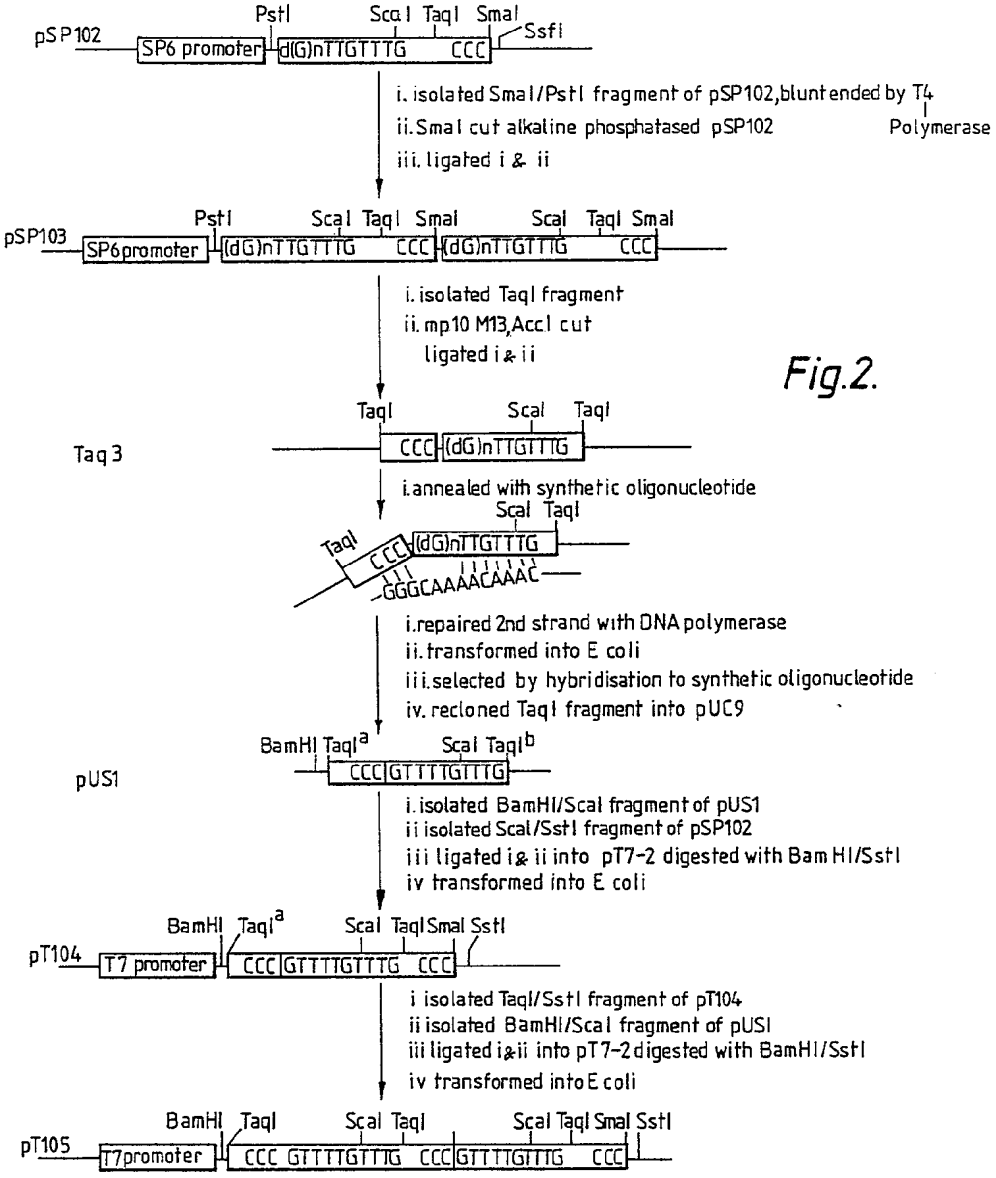

pSP102
PstI
ScaI TaqI SmaI
SsfI
SP6 promoter
d(G)nTTGTTTG CCC
i. isolated SmaI/PstI fragment of pSP102, blunt ended by T4 Polymerase
ii. SmaI cut alkaline phosphatased pSP102
iii. ligated i & ii
pSP103
PstI ScaI TaqI SmaI ScaI TaqI SmaI
SP6 promoter
(dG)nTTGTTTG CCC (dG)nTTGTTTG CCC
i. isolated TaqI fragment
ii. mp10 M13, AccI cut
ligated i & ii
TaqI ScaI TaqI
Taq 3
CCC (dG)nTTGTTTG
i. annealed with synthetic oligonucleotide
ScaI TaqI
TaqI
CCC (dG)nTTGTTTG
GGGCAAAACAAAC
i. repaired 2nd strand with DNA polymerase
ii. transformed into E coli
iii. selected by hybridisation to synthetic oligonucleotide
iv. recloned TaqI fragment into pUC9
BamHI TaqI[a] ScaI TaqI[b]
pUS1
CCC GTTTTGTTTG
i. isolated BamHI/ScaI fragment of pUS1
ii isolated ScaI/SstI fragment of pSP102
iii ligated i & ii into pT7-2 digested with BamHI/SstI
iv transformed into E coli
BamHI TaqI[a] ScaI TaqI SmaI SstI
pT104
T7 promoter
CCC GTTTTGTTTG CCC
i isolated TaqI/SstI fragment of pT104
ii isolated BamHI/ScaI fragment of pUSI
iii ligated i & ii into pT7-2 digested with BamHI/SstI
iv transformed into E coli
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pT105
T7promoter
CCC GTTTTGTTTG CCC GTTTTGTTTG CCC

Fig.2.

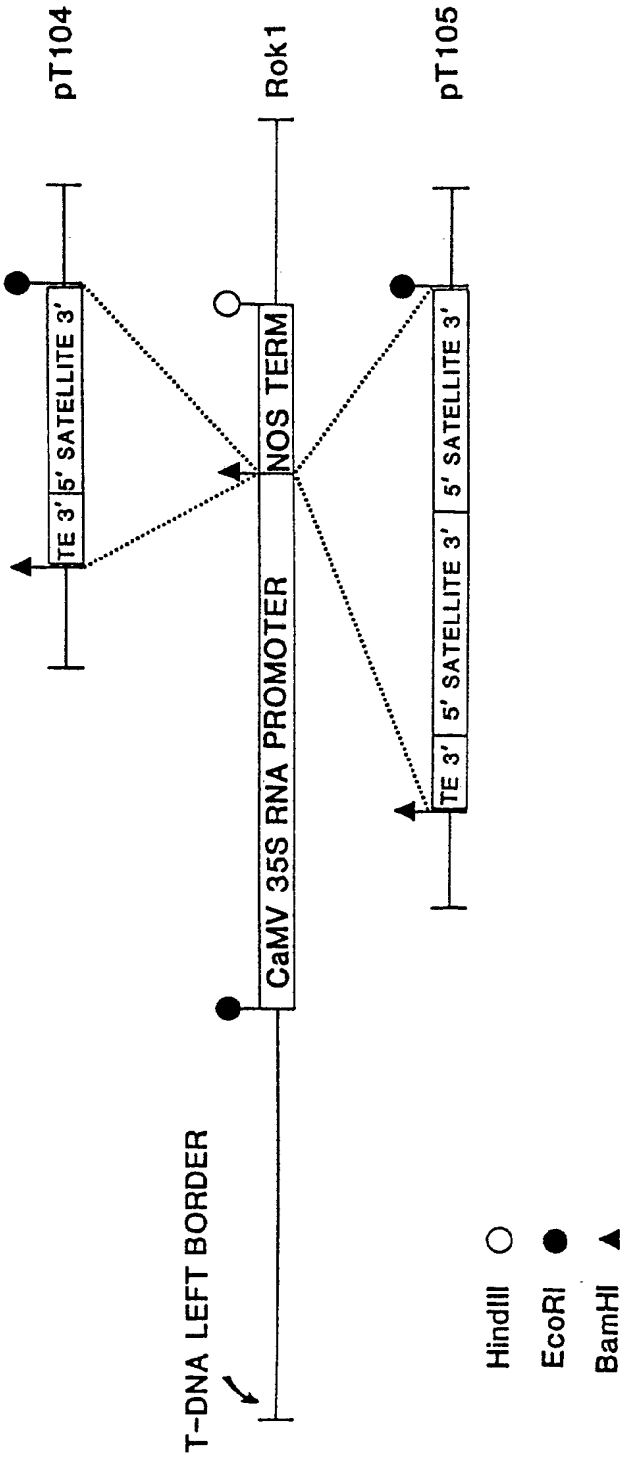
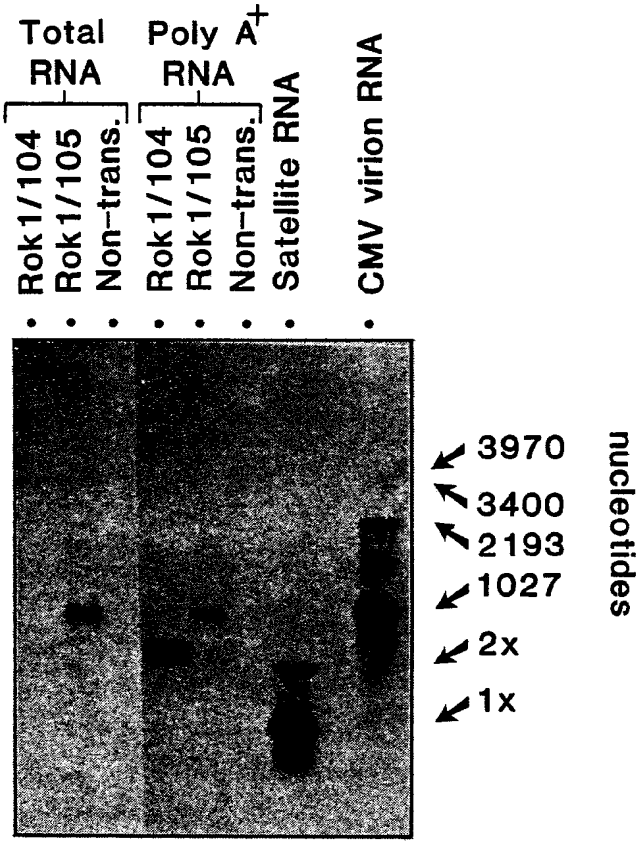

pT104
Rok1
pT105
TE 3'
5' SATELLITE 3'
CaMV 35S RNA PROMOTER
NOS TERM
T-DNA LEFT BORDER
HindIII
EcoRI
BamHI
500bp

Fig.3.

Fig. 4.


Total RNA
Poly A+ RNA
Rok1/104
Rok1/105
Non-trans.
Rok1/104
Rok1/105
Non-trans.
Satellite RNA
CMV virion RNA
3970
3400
2193
1027
2x
1x
nucleotides

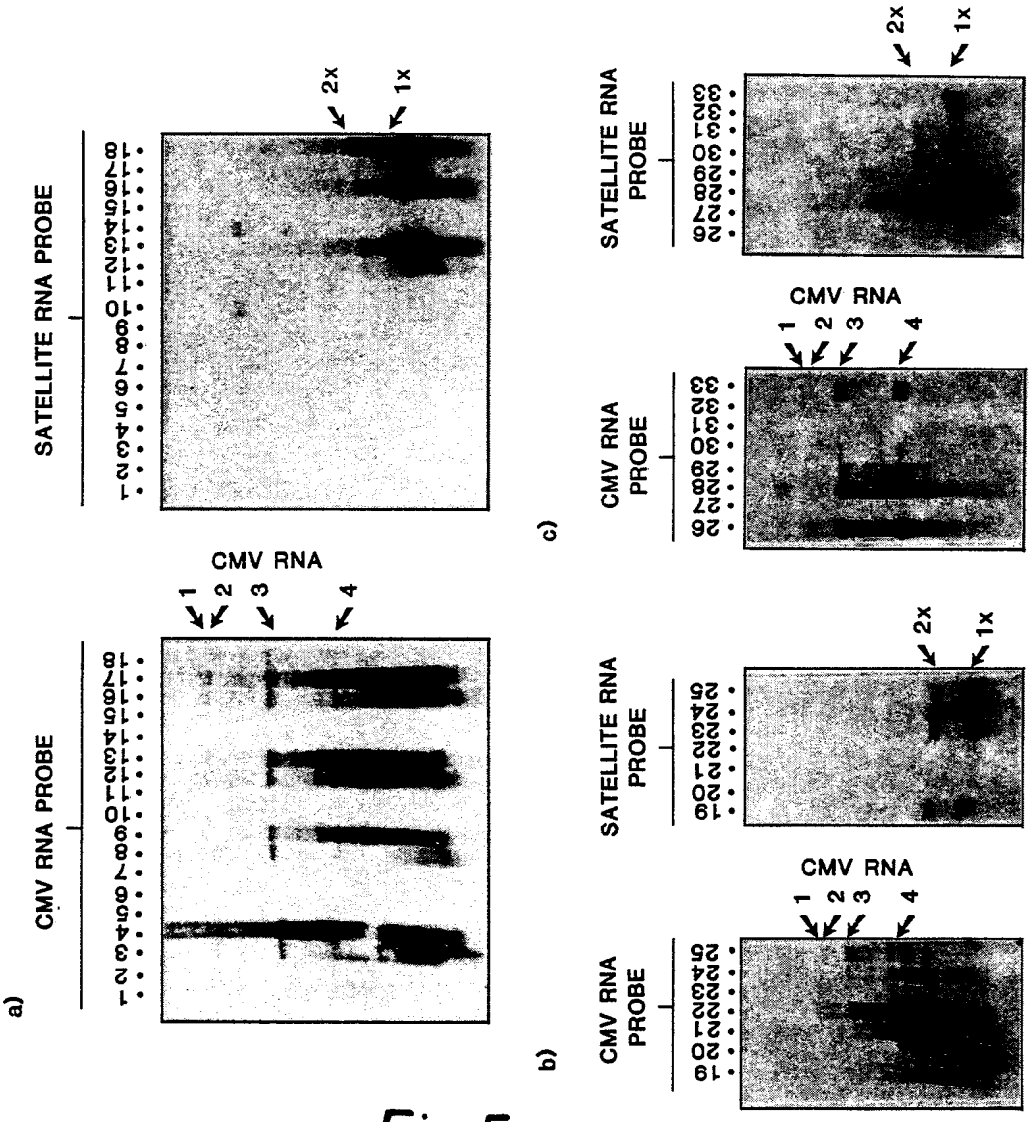

a)
CMV RNA PROBE
SATELLITE RNA PROBE
CMV RNA
1
2
3
4
2x
1x
b)
CMV RNA PROBE
SATELLITE RNA PROBE
CMV RNA
1
2
3
4
2x
1x
c)
CMV RNA PROBE
SATELLITE RNA PROBE
CMV RNA
1
2
3
4
2x
1x

Fig.5.

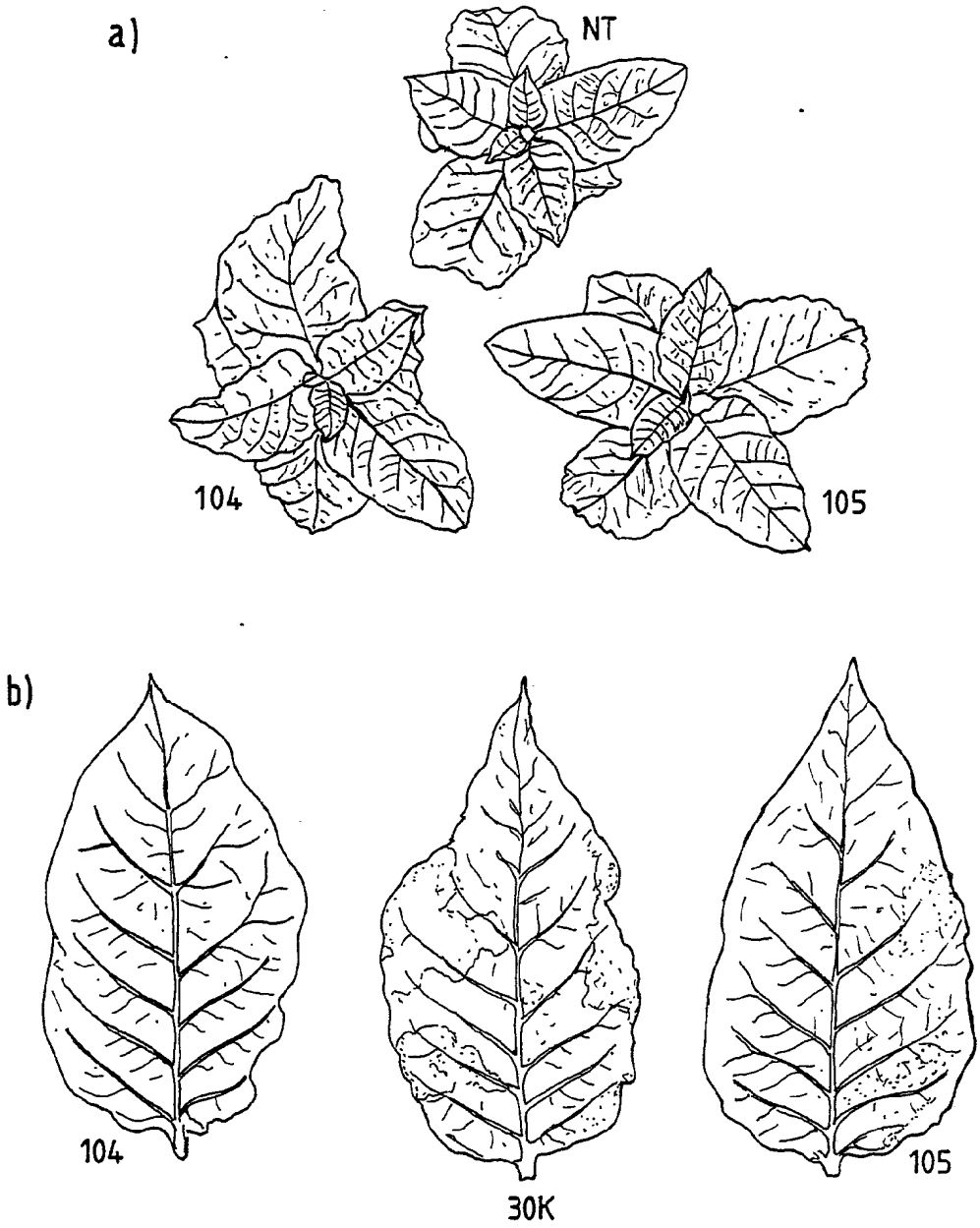


Fig.6.

European Patent Office

EUROPEAN SEARCH REPORT

Application number

DOCUMENTS CONSIDERED TO BE RELEVANT

EP 87300408.9

Category	Citation of document with indication, where appropriate, of relevant passages	Relevant to claim	CLASSIFICATION OF THE APPLICATION (Int. Cl.4)
A	EP - A1 - 0 149 430 (CIBA-GEIGY AG) * Claims 1,29 * --	1,2, 14,17	C 12 N 15/00 //(C 12 N 15/00 C 12 R 1:91)
A	EP - A1 - 0 159 418 (RIJKS-UNIVERSITEIT LEIDEN) * Claims 1,2 * --	1,10, 11	
A	EP - A1 - 0 164 575 (CIBA-GEIGY AG) * Abstract * ----	1	

TECHNICAL FIELDS SEARCHED (Int. Cl.4)

C 12 N

The present search report has been drawn up for all claims

Place of search	Date of completion of the search	Examiner
VIENNA	14-04-1987	WOLF

CATEGORY OF CITED DOCUMENTS

X : particularly relevant if taken alone
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